

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:48:53 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-10-786-850-1

Perfect score: 1603

Sequence: 1 AVPSQTQFWGKISYNDQSI.....GIGAGTGDDYAGFGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1179	73.5	431	2	Q9S3L6	Q9S3L6 bacillus sp
2	1170	73.0	434	2	O54327	O54327 bacillus sp
3	1123	70.1	416	2	Q6W4N2	Q6W4N2 bacillus sp
4	1091.5	68.1	419	2	Q45681	Q45681 bacillus su
5	1050.5	65.5	420	1	SUBT_BACSN	P23842 bacillus sp
6	726.5	45.3	425	2	Q647R6	Q647R6 uncultured
7	477	29.8	374	2	Q9F943	Q9F943 bacillus li
8	474	29.6	310	2	Q9PDF2	Q9PDF2 bacillus li
9	474	29.6	310	2	Q9PDF3	Q9PDF3 bacillus li
10	474	29.6	374	2	Q9F941	Q9F941 bacillus li
11	474	29.6	374	2	Q9F942	Q9F942 bacillus li
12	474	29.6	379	2	Q9ECN9	Q9ECN9 bacillus mo
13	474	29.6	379	2	Q6PNN5	Q6PNN5 bacillus li
14	472	29.4	379	1	SUBT_BACLI	P00780 bacillus li
15	472	29.4	379	2	Q9PDF4	Q9PDF4 bacillus li
16	472	29.4	379	2	Q6SLP7	Q6SLP7 bacillus li
17	471	29.4	379	2	Q45300	Q45300 bacillus li
18	470	29.3	310	2	Q9F7C2	Q9F7C2 bacillus li
19	470	29.3	379	2	Q53521	Q53521 bacillus li
20	468	29.2	379	2	Q45301	Q45301 bacillus li
21	463.5	28.9	269	1	PRTM_BACSK	Q99405 bacillus sp
22	460	28.7	379	2	Q66153	Q66153 bacillus sp
23	458.5	28.6	404	2	Q76L29	Q76L29 bacillus sp
24	456.5	28.5	269	1	SUBS_BACLE	P23600 bacillus le
25	456.5	28.5	380	1	ELYA_BACAO	P27693 bacillus al
26	456.5	28.5	380	1	ELYA_BACCS	P41362 bacillus cl
27	455	28.4	274	1	SUBD_BACLI	P00781 bacillus li
28	454	28.3	374	2	Q45523	Q45523 bacillus sp
29	454	28.3	378	2	Q45466	Q45466 bacillus sp
30	447.5	27.9	382	2	Q45522	Q45522 bacillus sp
31	446.5	27.9	376	2	Q76KL9	Q76KL9 bacillus sp

ALIGNMENTS

RESULT 1

Q9S3L6

ID Q9S3L6 PRELIMINARY; PRT; 431 AA.
AC Q9S3L6; TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative 36kDa protease.
OS Bacillus sphaericus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1421;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2297;
RX MEDLINE=99318657; PubMed=10388698;
RA Servant P., Rosso M.L., Hamon S., Poncet S., Delecluse A.,
RA Rapoport G.;
RT "Production of CryIIA and CryIIb toxins in Bacillus sphaericus
confers toxicity towards Aedes aegypti and resistant Culex
populations.";
RT Appl. Environ. Microbiol. 65:3021-3026(1999).
CC -1- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; AJ238598; CAB46075.1; -;
DR PDB; 1EA7; X-ray; A=122-431.
DR MEROPS; S08.113; -;
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004239; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease, Serine protease.
SQ SEQUENCE 431 AA; 45345 MW; C1CFEAE71C2C6D2 CRC64;

Query Match 73.5%; Score 1179; DB 2; Length 431;

Best Local Similarity 73.1%; Pred. No. 1e-69;

Matches 225; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 4 STQFWGKISYNDQSIKTKTGSGIKVAVLDTGYTSHLGLAGSAEQCKDFTQSNPLVD 63

Db 124 SQQIPWGKIKAYNNDTLTSTTGGSGINIAVLDTGWTSHPLVNNVEQCKDFTGATPIN 183

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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:56:59 ; Search time 41 Seconds
(without alignments)
729,839 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPSQTTPWGIKSIYNDQSI.....GIGACTGDDYASGFGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : PIR_79:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1091.5	68.1	419	1 S25835	subtilisin (EC 3.4
2	1050.5	65.5	420	1 S23407	subtilisin (EC 3.4
3	472	29.1	379	1 SUBSCL	subtilisin (EC 3.4
4	466	29.1	275	2 JCI085	subtilisin (EC 3.4
5	456.5	28.5	380	2 A49778	high-alkaline seri
6	455	28.4	274	1 SUBSD	subtilisin (EC 3.4
7	454	28.3	374	2 I39781	subtilisin (EC 3.4
8	447.5	27.9	382	2 I39780	subtilisin (EC 3.4
9	446	27.8	378	2 A33973	high-alkaline seri
10	443.5	27.7	361	2 G83756	subtilisin-type al
11	439.5	27.4	382	1 SUBSN	subtilisin (EC 3.4
12	438.5	27.4	361	2 A48373	high-alkaline seri
13	425.5	26.5	381	1 SUBSS	subtilisin (EC 3.4
14	425.5	26.5	381	2 JQ1487	subtilisin (EC 3.4
15	422.5	26.4	272	2 A23624	subtilisin (EC 3.4
16	422.5	26.4	381	2 JH0778	subtilisin (EC 3.4
17	421.5	26.3	381	1 SUBSI	subtilisin (EC 3.4
18	416	26.0	384	2 J46802	alkaline proteinase
19	415	25.9	401	2 A57690	aerolysin precursor
20	409	25.5	397	2 JW0075	cysteine-dependent
21	408	25.5	279	1 SUMYTV	thermitase (EC 3.4
22	403	25.1	613	2 S75976	hypothetical prote
23	402	25.1	401	2 I39974	serine proteinase
24	398.5	24.9	534	1 J50173	alkaline proteinase
25	388.5	24.2	488	2 A11930	proteinase (import
26	384.5	24.0	525	2 G84406	halolysin (importe
27	381.5	23.8	321	1 S27501	alkaline proteinase
28	381.5	23.8	645	1 SUBSMP	serine proteinase
29	377.5	23.5	372	2 D83735	subtilisin-type al

30	373	23.3	319	2 I39866	microbial serine p
31	370.5	23.1	436	2 I39973	alkaline serine pr
32	367.5	22.9	535	2 B82358	alkaline serine pr
33	364.5	22.7	293	2 JQ0380	proteinase T (EC 3
34	360	22.5	530	2 A42605	halolysin (EC 3.4
35	357.5	22.3	440	2 H72784	probable alkaline
36	356.5	22.2	513	1 A35742	aqualysin (EC 3.4
37	354.5	22.1	326	1 C41335	microbial serine p
38	354	22.1	388	1 S22387	microbial serine p
39	354	22.1	519	2 S71451	cuticle-degrading
40	353	22.0	384	1 SUTIKA	halolysin R4 (EC 3
41	345.5	21.6	615	2 A42248	endopeptidase K (E
42	340	21.2	393	2 T36842	proteinase (import
43	340	21.2	806	2 A41341	probable secreted
44	338	21.1	536	2 JC7826	microbial serine p
45	337.5	21.1	409	1 S32905	serine proteinase
46	337	21.0	588	2 C83836	subtilisin-type pr
47	334.5	20.9	442	2 A69587	intracellular alka
48	334	20.8	894	2 F69730	cell wall-associat
49	333	20.8	387	2 S11985	serine proteinase
50	331	20.6	379	1 JC2142	alkaline proteinase
51	329.5	20.6	322	2 G83922	intracellular alka
52	328	20.5	757	2 C84120	subtilisin-type pr
53	326.5	20.4	323	2 I39867	microbial serine p
54	326	20.3	1448	2 A12007	Subtilase family p
55	325	20.3	591	2 A75474	serine proteinase,

ALIGNMENTS

RESULT 1

S25835 subtilisin (EC 3.4.21.62) precursor - Bacillus sp. (strain TA41)

C:Species: Bacillus sp.

C:Date: 22-Nov-1993 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999

C:Accession: S25835

R:Davall, S.; Feller, G.; Narinx, B.; Gerday, C.

Gene 119, 143-144, 1992

A:Title: Sequence of the subtilisin-encoding gene from an antarctic psychrotroph Bacil

A:Reference number: S25835; MUID:93012966; PMID:1398082

A:Accession: S25835

A:Molecule type: DNA

A:Residues: 1-419 <DAV>

A:Cross-references: EMBL:X63533; NID:940198; PIDN:CAA45096.1; PID:G40199

C:Superfamily: subtilisin; subtilisin homology

C:Keywords: extracellular protein; hydrolase; serine proteinase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-110/Domain: propeptide #status predicted <PRO>

F:111-419/Product: microbial serine proteinase #status predicted <MAT>

F:135-373/Domain: subtilisin homology <SRT>

F:144,184,359/Active site: Asp, His, Ser #status predicted

Query Match 68.1%; Score 1091.5; DB 1; Length 419;
Best Local Similarity 67.5%; Pred. No. 7.4e-66;
Matches 208; Conservative 41; Mismatches 58; Indels 1; Gaps 1;

Qy	4	STQTPWGIKSIYNDQSIKTGTGGSGIKVAVLDGTGYTSHLDLAGSAEOKDPTQSNPLVD 63
Db	113	SQSTPWGIKALYNNSLTSTSGGAGINIAVLDTGVTNHPDLSNNVBOCKDFTVGTNFTD 172
Qy	64	GSCTDRQGHGTHVAGTVLAHSGNSGQGVYVAPQAKLWAYKVLGNDGSGYSDDIAAALRH 123
Db	173	NSCTDRQGHGTHVAGSALANGT-GSGYGVVAPADLWAYKVLGDDGSGYADDIAALRH 231
Qy	124	VADASTGTGKVINMISGLSAKOSLIASAVDYAYGKVLIVAAAGNSGSGNTTGFPGG 183
Db	232	AGDQATALNTKVINMISGLSGSSSLITNAVDYAYDKGLVIAAAGNSGPKFGSIGYPGA 291
Qy	184	LVNAVAALNTVOONTYRVADPSSRCNPATAGDYIIQERDIEVSAPGASVESTWYGG 243
Db	292	LVNAVAALNTTQNTYRVADPSSRHGRKRTAGDYVIQKGDVBIAPGAAYVSTWFDGG 351

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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:48:08 ; Search time 166 Seconds
(without alignments)
724.593 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPSTQTPWGKSIYNDQSI.....GIGAGTGDDYASGFGYPRVK 311

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1603	100.0	311	8 ADR05440	Adr05440 TY145 sub
2	1603	100.0	311	8 ADR05388	Adr05388 TY145 sub
3	1603	100.0	311	8 ADS52006	Ads52006 Bacillus
4	1603	100.0	418	5 ABB77095	Abb77095 Bacillus
5	1179	73.5	310	8 ADR05391	Adr05391 Bacillus
6	1179	73.5	310	8 ADR05439	Adr05439 Bacillus
7	1091.5	68.1	309	8 ADR05441	Adr05441 TA41 sub
8	1091.5	68.1	419	8 ADR05390	Adr05390 TA41 sub
9	1050.5	65.5	309	8 ADR05442	Adr05442 TA39 sub
10	1050.5	65.5	420	8 ADR05389	Adr05389 TA39 sub
11	487.5	30.4	269	4 AAG66802	Aag66802 Novel sub
12	479	29.9	274	2 AAR11003	Aar11003 Alkaline
13	477	29.8	372	6 AAE22942	Aae22942 Bacillus
14	476	29.7	274	2 AAW15457	Aaw15457 Subtilisin
15	475	29.6	274	2 AAR10451	Aar10451 C002 muta
16	475	29.6	274	2 AAW15441	Aaw15441 Subtilisin
17	475	29.6	274	2 AAW15447	Aaw15447 Subtilisin
18	474.5	29.6	377	2 AAR34259	Aar34259 Bacillus
19	474	29.6	274	2 AAR11005	Aar11005 Alkaline
20	474	29.6	274	4 ABM00034	Abm00034 Alcalase
21	474	29.6	310	6 AAE22948	Aae22948 Bacillus
22	473	29.5	274	1 AAP80273	Aap80273 Amino aci
23	473	29.5	274	1 AAR27790	Aar27790 B. lichen
24	473	29.5	274	2 AAW15451	Aaw15451 Subtilisin
25	473	29.5	274	2 AAW15454	Aaw15454 Subtilisin

26	473	29.5	274	2 AAW00080	Aaw00080 Alkaline
27	473	29.5	274	2 AAY24910	Aay24910 Carlsberg
28	473	29.5	274	2 AAY08312	Aay08312 B. lichen
29	473	29.5	274	2 AAW82795	Aaw82795 B. lichen
30	473	29.5	274	2 AAY08317	Aay08317 B. lichen
31	473	29.5	274	3 AAB02975	Aab02975 Bacillus
32	473	29.5	274	3 AAY77003	Aay77003 Bacillus
33	473	29.5	274	3 AAB03774	Aab03774 Subtilisin
34	473	29.5	274	4 AAU38519	Aau38519 Subtilisin
35	473	29.5	274	5 ABB75075	Abb75075 Bacillus
36	473	29.5	274	5 ABG91095	Abg91095 Subtilisin
37	473	29.5	274	6 ABP54392	Abp54392 Bacillus
38	473	29.5	274	7 ADE25792	Ad25792 B. lichen
39	473	29.5	274	7 ADE81096	Ad81096 Bacillus
40	473	29.5	274	7 ADF66224	Adf66224 B. lichen
41	473	29.5	274	8 ADH69158	Adh69158 B. lichen
42	473	29.5	274	8 ADJ77874	Adj77874 B. lichen
43	473	29.5	274	8 ADJ46871	Adj46871 B. lichen
44	473	29.5	274	8 ADO04602	Ado04602 Bacillus
45	472.5	29.5	383	5 ADE54158	Ad54158 L-25 kera
46	472	29.4	274	1 AAP90377	Aap90377 Subtilisin
47	472	29.4	274	3 AAB11907	Aab11907 Mature wi
48	472	29.4	274	4 AAB62485	Aab62485 Amino aci
49	472	29.4	274	4 AAB62487	Aab62487 Amino aci
50	472	29.4	274	6 ABR63751	Ab63751 Bacillus
51	472	29.4	274	6 ABR63735	Ab63735 Bacillus
52	472	29.4	274	7 ABR63726	Ab63726 B licheni
53	472	29.4	274	7 ABR63648	Ab63648 B licheni
54	472	29.4	274	7 ADC18496	Adc18496 Bacillus
55	472	29.4	274	7 ADD85940	Add85940 Bacillus

ALIGNMENTS

RESULT 1

ADR05440 ID ADR05440 standard; protein; 311 AA.
XX AC ADR05440;
XX DT 04-NOV-2004 (first entry)
XX DE TY145 subtilase amino acid sequence.
XX KW Subtilisin family subtilase; subtilase; enzyme; subtilase variant;
KW three-dimensional structure; 3D structure; protein co-ordinate data;
KW Thr-Tyr145 subtilase; TY145 subtilase; ion-binding site; detergent;
KW cleaning; washing.
XX OS Bacillus sp.
XX OS Synthetic.
XX PN WO2004067737-A2.
XX PD 12-AUG-2004.
XX PF 30-JAN-2004; 2004WO-DK000066.
XX PR 30-JAN-2003; 2003DK-00000119.
XX PR 05-FEB-2003; 2003US-0445300P.
XX PR 07-MAY-2003; 2003DK-00000689.
XX PA (NOVO) NOVOZYMES AS.
XX PI Svendsen A, Draborg H;
XX DR WPI; 2004-594206/57.
XX PT Producing variant of parent Subtilisin family subtilase which are useful
PT in washing and cleaning applications. Involves use of three-dimensional
PT model of known subtilases for identifying and modifying parts structural
PT parts of parent.

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 21:07:05 ; Search time 163 Seconds
(without alignments)
752.566 Million cell updates/sec

Title: US-10-786-850-1

Perfect score: 1603

Sequence: 1 AVPTQTWGIKSIYNDQSI.....GIGAGTGDYAGRGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1603	100.0	311	16 US-10-786-850-1	Sequence 1, Appli
2	1603	100.0	418	9 US-09-966-921A-2	Sequence 2, Appli
3	1179	73.5	310	16 US-10-786-850-4	Sequence 4, Appli
4	1091.5	68.1	419	16 US-10-786-850-3	Sequence 3, Appli
5	1050.5	65.5	420	16 US-10-786-850-2	Sequence 2, Appli
6	477	29.8	372	10 US-09-813-408-9	Sequence 9, Appli
7	474	29.6	274	12 US-09-957-806A-25	Sequence 25, Appli
8	474	29.6	274	12 US-09-957-806A-45	Sequence 45, Appli
9	474	29.6	310	10 US-09-813-408-15	Sequence 15, Appli
10	473	29.5	274	8 US-08-322-678-9	Sequence 9, Appli
11	473	29.5	274	9 US-09-060-854B-5	Sequence 5, Appli

12	473	29.5	274	14	US-10-033-325-5	Sequence 5, Appli
13	473	29.5	274	14	US-10-104-693-5	Sequence 5, Appli
14	473	29.5	274	14	US-10-228-572-5	Sequence 5, Appli
15	473	29.5	274	14	US-10-324-152-4	Sequence 5, Appli
16	473	29.5	274	15	US-10-423-649-5	Sequence 5, Appli
17	473	29.5	274	15	US-10-323-324-9	Sequence 9, Appli
18	473	29.5	274	15	US-10-685-689-4	Sequence 4, Appli
19	473	29.5	274	15	US-10-614-370-9	Sequence 9, Appli
20	473	29.5	274	18	US-10-924-092A-5	Sequence 5, Appli
21	473	29.5	274	20	US-11-020-628-5	Sequence 5, Appli
22	472	29.4	274	14	US-10-242-549-6	Sequence 6, Appli
23	472	29.4	274	14	US-10-313-853-4	Sequence 4, Appli
24	472	29.4	274	14	US-10-243-576-6	Sequence 6, Appli
25	472	29.4	274	17	US-10-872-166-12	Sequence 12, Appli
26	472	29.4	274	17	US-10-836-959-19	Sequence 19, Appli
27	472	29.4	274	17	US-10-873-917-10	Sequence 10, Appli
28	472	29.4	274	17	US-10-873-610-10	Sequence 10, Appli
29	472	29.4	274	17	US-10-872-162-16	Sequence 16, Appli
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31	472	29.4	274	10	US-09-813-408-11	Sequence 11, Appli
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33	472	29.4	274	15	US-10-146-905A-12	Sequence 12, Appli
34	471	29.4	276	14	US-10-243-576-35	Sequence 35, Appli
35	471	29.4	276	14	US-10-243-576-37	Sequence 37, Appli
36	471	29.4	276	14	US-09-813-408-13	Sequence 13, Appli
37	470	29.3	276	14	US-10-243-576-33	Sequence 33, Appli
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41	469	29.3	276	14	US-10-243-576-27	Sequence 27, Appli
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43	469	29.3	276	14	US-10-243-576-31	Sequence 31, Appli
44	469	29.3	276	14	US-09-920-118-14	Sequence 14, Appli
45	466	29.1	276	14	US-10-243-576-23	Sequence 23, Appli
46	466	29.1	276	14	US-10-243-576-25	Sequence 25, Appli
47	463.5	28.9	269	17	US-10-873-917-3	Sequence 3, Appli
48	463.5	28.9	269	17	US-10-873-917-2	Sequence 2, Appli
49	463	28.9	270	12	US-09-957-806A-32	Sequence 32, Appli
50	463	28.9	270	12	US-09-957-806A-55	Sequence 55, Appli
51	460.5	28.7	378	10	US-09-813-408-14	Sequence 14, Appli
52	460.5	28.7	380	10	US-09-824-893A-261	Sequence 261, App
53	460.5	28.7	380	16	US-10-736-397-261	Sequence 261, App
54	459.5	28.7	271	14	US-10-243-576-34	Sequence 34, Appli
55	458.5	28.6	271	14	US-10-243-576-36	Sequence 36, Appli

ALIGNMENTS

RESULT 1
US-10-786-850-1
; Sequence 1, Application US/10786850
; Publication No. US20040209343A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Draborg, Henriette
; TITLE OF INVENTION: Subtilase variants
; FILE REFERENCE: 10203
; CURRENT APPLICATION NUMBER: US/10/786,850
; CURRENT FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 311
; TYPE: PRT
; ORGANISM: TYL45 subtilase
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(311)
US-10-786-850-1

Query Match 100.0%; Score 1603; DB 16; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 20:58:19 ; Search time 43 Seconds
(without alignments)
539,904 Million cell updates/sec

Title: US-10-786-850-1
Perfect score: 1603
Sequence: 1 AVPSTQTPWGIKSIYNDQSI.....GIGACTGDDYASGFGYPRVK 311

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 55 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1082	67.5	418	2	US-08-873-479-44
3	487.5	30.4	269	4	US-09-533-480C-2
4	474.5	29.6	377	1	US-07-772-087-2
5	473	29.5	274	1	US-08-322-677A-9
6	473	29.5	274	1	US-08-322-676-9
7	473	29.5	274	2	US-09-135-658-2
8	473	29.5	274	3	US-08-898-218-9
9	473	29.5	274	3	US-08-848-793-9
10	473	29.5	274	3	US-09-255-502-4
11	473	29.5	274	3	US-09-178-155-5
12	473	29.5	274	3	US-09-445-270-4
13	473	29.5	274	4	US-08-400-698-1
14	473	29.5	274	4	US-09-178-173A-5
15	473	29.5	274	4	US-08-322-678-9
16	473	29.5	274	4	US-09-255-501-5
17	473	29.5	274	4	US-09-060-854B-5
18	473	29.5	274	4	US-09-177-353-5
19	473	29.5	274	4	US-10-033-325-5
20	473	29.5	274	4	US-09-529-904-6
21	473	29.5	274	4	US-09-060-872A-5
22	473	29.5	274	4	US-09-500-135C-5
23	472	29.4	274	1	US-08-431-387-2
24	472	29.4	274	2	US-08-865-203-7
25	472	29.4	274	2	US-07-849-420-7
26	472	29.4	274	3	US-09-253-854-7
27	472	29.4	274	3	US-08-955-424-7

28	472	29.4	274	4	US-10-242-549-6	Sequence 6, Appli
29	472	29.4	274	4	US-10-243-576-6	Sequence 6, Appli
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32	472	29.4	378	1	US-07-772-087-4	Sequence 4, Appli
33	472	29.4	379	2	US-08-845-295A-1	Sequence 1, Appli
34	472	29.4	379	3	US-09-140-933-1	Sequence 1, Appli
35	472	29.4	379	3	US-09-146-661-1	Sequence 1, Appli
36	472	29.4	379	3	US-09-150-515-1	Sequence 1, Appli
37	471	29.4	276	4	US-10-243-576-35	Sequence 35, Appli
38	470	29.3	276	4	US-10-243-576-37	Sequence 37, Appli
39	470	29.3	276	4	US-10-243-576-33	Sequence 33, Appli
40	470	29.3	379	1	US-08-685-774-2	Sequence 2, Appli
41	469	29.3	276	4	US-10-243-576-27	Sequence 27, Appli
42	469	29.3	276	4	US-10-243-576-29	Sequence 29, Appli
43	469	29.3	276	4	US-10-243-576-31	Sequence 31, Appli
44	468.5	29.2	275	6	5472855-5	Patent No. 5472855
45	468.5	29.2	275	6	5472855-5	Patent No. 5472855
46	466	29.1	276	4	US-10-243-576-23	Sequence 23, Appli
47	466	29.1	276	4	US-10-243-576-25	Sequence 25, Appli
48	459.5	28.7	269	1	US-07-706-691G-50	Sequence 50, Appli
49	459.5	28.7	269	1	US-08-254-021-50	Sequence 50, Appli
50	459.5	28.7	269	2	US-08-618-446-50	Sequence 50, Appli
51	459.5	28.7	269	3	US-08-980-135-50	Sequence 50, Appli
52	459.5	28.7	269	4	US-09-585-798-50	Sequence 50, Appli
53	459.5	28.7	271	4	US-10-243-576-34	Sequence 34, Appli
54	458.5	28.6	271	4	US-10-243-576-36	Sequence 36, Appli
55	458.5	28.6	271	4	US-10-243-576-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1

US-09-966-921A-2
; Sequence 2, Application US/09966921A
; Patent No. 6511371
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Lassen, Soren
; APPLICANT: Pedersen, Poul
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides Having Proteolytic Activity
; FILE REFERENCE: 10097.200-US
; CURRENT APPLICATION NUMBER: US/09/966,921A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-966-921A-2

Query Match 100.0%; Score 1603; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 5.7e-120;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	108	AVPSTQTPWGIKSIYNDQSIITKTGGSGIKVAVLDTGVYTSKVLHLAGSAEQCKDFTQSNP	167
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Qy	121	IRHVADEASRTGSKVIVNNSLGSSAKOSLIASAVDYAYKGVLIIVAAAGNSGSGNTIGF	180
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Db	288	PGGLVNAVAALENVQNGTYRVADFSRGNPATAGDYIIQERDIEVSAPGASVESTWY	347